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RAW SEQUENCE LISTING   DATE: 12/19/2000
PATENT APPLICATION: US/09/729,264   TIME: 07:27:30

Input Set : A:\A-692.ST25.txt
Output Set: N:\CRF3\12192000\I729264.raw

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 3 <110> APPLICANT: WELCHER, ANDREW
 4         SARMIENTO, ULLA
 5         SCHULTZ, HENRY
 6         CHUTE, HILARY
 8 <120> TITLE OF INVENTION: B7-LIKE MOLECULES AND USES THEREOF
10 <130> FILE REFERENCE: A-692
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/729,264
13 <141> CURRENT FILING DATE: 2000-11-28
15 <150> PRIOR APPLICATION NUMBER: US 60/214,512
16 <151> PRIOR FILING DATE: 2000-06-28
18 <160> NUMBER OF SEQ ID NOS: 15
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1175
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (27)..(1172)
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33                              Met Gly Leu Val Ile Phe Leu His Gly
34                               1               5
36 tct ggg tct ggt aat gaa gtc ata gaa ggc ccc cag aat gca aca gtc   101
37 Ser Gly Ser Gly Asn Glu Val Ile Glu Gly Pro Gln Asn Ala Thr Val
38  10              15                  20                  25
40 ctg aag ggc tcc cag gct cgc ttc aac tgc acc gtc tcc cag ggc tgg   149
41 Leu Lys Gly Ser Gln Ala Arg Phe Asn Cys Thr Val Ser Gln Gly Trp
42              30                  35                  40
44 aag ctc atc atg tgg gct ctc agt gac atg gtg gtg cta agc gtc agg   197
45 Lys Leu Ile Met Trp Ala Leu Ser Asp Met Val Val Leu Ser Val Arg
46              45                  50                  55
48 ccc atg gag ccc atc atc acc aat gac cgc ttc acc tct cag agg tac   245
49 Pro Met Glu Pro Ile Ile Thr Asn Asp Arg Phe Thr Ser Gln Arg Tyr
50          60                  65                  70
52 gac cag ggc ggg aac ttc acc tcg gag atg atc atc cac aat gtg gag   293
53 Asp Gln Gly Gly Asn Phe Thr Ser Glu Met Ile Ile His Asn Val Glu
54      75                  80                  85
56 ccc agt gat tcg ggg aac atc aga tgc agc ctc cag aac agt cgc ctg   341
57 Pro Ser Asp Ser Gly Asn Ile Arg Cys Ser Leu Gln Asn Ser Arg Leu
58  90                  95                 100                 105
60 cat gga tct gct tac ctt acc gtc caa gtt atg gga gag ctg ttc att   389
61 His Gly Ser Ala Tyr Leu Thr Val Gln Val Met Gly Glu Leu Phe Ile
62              110                 115                 120
64 ccc agt gtt aat ctt gta gtc gct gag aat gaa cct tgt gaa gtt act   437
65 Pro Ser Val Asn Leu Val Val Ala Glu Asn Glu Pro Cys Glu Val Thr
66              125                 130                 135
```

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68  tgt cta ccc tca cac tgg acc cgg ctc ccg gat att tcc tgg gag ctc      485
69  Cys Leu Pro Ser His Trp Thr Arg Leu Pro Asp Ile Ser Trp Glu Leu
70          140             145             150
72  ggt ctc ctg gtc agc cat tca agc tat tat ttt gtt ccg gag ccc agc      533
73  Gly Leu Leu Val Ser His Ser Ser Tyr Tyr Phe Val Pro Glu Pro Ser
74          155             160             165
76  gac ctt caa agt gca gtg agc atc ctg gct ctg acc cca cag agc aat      581
77  Asp Leu Gln Ser Ala Val Ser Ile Leu Ala Leu Thr Pro Gln Ser Asn
78  170             175             180             185
80  ggg act ttg act tgc gtg gct acc tgg aag agc ctg aag gcc cgc aag      629
81  Gly Thr Leu Thr Cys Val Ala Thr Trp Lys Ser Leu Lys Ala Arg Lys
82          190             195             200
84  tct gca act gta aat ctc act gtg att cgg tgt ccc caa gac act gga      677
85  Ser Ala Thr Val Asn Leu Thr Val Ile Arg Cys Pro Gln Asp Thr Gly
86          205             210             215
88  ggt ggt att aat att cca ggt gta tta tca agt tta ccg agt tta ggt      725
89  Gly Gly Ile Asn Ile Pro Gly Val Leu Ser Ser Leu Pro Ser Leu Gly
90          220             225             230
92  ttt tca ttg cct act tgg ggc aaa gtt gga ctt gga cta gca ggc acc      773
93  Phe Ser Leu Pro Thr Trp Gly Lys Val Gly Leu Gly Leu Ala Gly Thr
94          235             240             245
96  atg ctt ctg acg ccg acg tgt act ctt aca ata cgc tgc tgc tgc tgc      821
97  Met Leu Leu Thr Pro Thr Cys Thr Leu Thr Ile Arg Cys Cys Cys Cys
98  250             255             260             265
100 cgc cgt cgt tgt tgt ggc tgc aac tgc tgc tgc cgt tgt tgt ttc tgc      869
101 Arg Arg Arg Cys Cys Gly Cys Asn Cys Cys Cys Arg Cys Cys Phe Cys
102             270             275             280
104 tgt aga aga aaa aga gga ttt cgt att caa ttt caa aag aaa tct gaa      917
105 Cys Arg Arg Lys Arg Gly Phe Arg Ile Gln Phe Gln Lys Lys Ser Glu
106             285             290             295
108 aaa gag aag aca aac aaa gaa act gag aca gaa agt gga aat gaa aac      965
109 Lys Glu Lys Thr Asn Lys Glu Thr Glu Thr Glu Ser Gly Asn Glu Asn
110         300             305             310
112 tcc ggc tac aat tca gat gaa caa aag acc aca gac acc gct tct ctc     1013
113 Ser Gly Tyr Asn Ser Asp Glu Gln Lys Thr Thr Asp Thr Ala Ser Leu
114         315             320             325
116 cct ccc aaa tcc tgt gaa tcc agt gat cct gaa caa aga aac agt agc     1061
117 Pro Pro Lys Ser Cys Glu Ser Ser Asp Pro Glu Gln Arg Asn Ser Ser
118 330             335             340             345
120 tgt ggc cct cct cac cag cgg gct gat caa cgt cca ccc agg cca gca     1109
121 Cys Gly Pro Pro His Gln Arg Ala Asp Gln Arg Pro Pro Arg Pro Ala
122             350             355             360
124 agt cat cca cag gct tct ttt aat ctg gcc agt cct gag aag gtc agt     1157
125 Ser His Pro Gln Ala Ser Phe Asn Leu Ala Ser Pro Glu Lys Val Ser
126             365             370             375
128 aat aca act gta gta tag                                             1175
129 Asn Thr Thr Val Val
130             380
133 <210> SEQ ID NO: 2
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134 <211> LENGTH: 382
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 2
140 Met Gly Leu Val Ile Phe Leu His Gly Ser Gly Ser Gly Asn Glu Val
141 1               5                  10                  15
144 Ile Glu Gly Pro Gln Asn Ala Thr Val Leu Lys Gly Ser Gln Ala Arg
145             20                  25                  30
148 Phe Asn Cys Thr Val Ser Gln Gly Trp Lys Leu Ile Met Trp Ala Leu
149         35                  40                  45
152 Ser Asp Met Val Val Leu Ser Val Arg Pro Met Glu Pro Ile Ile Thr
153     50                  55                  60
156 Asn Asp Arg Phe Thr Ser Gln Arg Tyr Asp Gln Gly Gly Asn Phe Thr
157 65                  70                  75              80
160 Ser Glu Met Ile Ile His Asn Val Glu Pro Ser Asp Ser Gly Asn Ile
161                 85                  90                  95
164 Arg Cys Ser Leu Gln Asn Ser Arg Leu His Gly Ser Ala Tyr Leu Thr
165             100                 105                 110
168 Val Gln Val Met Gly Glu Leu Phe Ile Pro Ser Val Asn Leu Val Val
169             115                 120                 125
172 Ala Glu Asn Glu Pro Cys Glu Val Thr Cys Leu Pro Ser His Trp Thr
173     130                 135                 140
176 Arg Leu Pro Asp Ile Ser Trp Glu Leu Gly Leu Leu Val Ser His Ser
177 145                 150                 155             160
180 Ser Tyr Tyr Phe Val Pro Glu Pro Ser Asp Leu Gln Ser Ala Val Ser
181             165                 170                 175
184 Ile Leu Ala Leu Thr Pro Gln Ser Asn Gly Thr Leu Thr Cys Val Ala
185             180                 185                 190
188 Thr Trp Lys Ser Leu Lys Ala Arg Lys Ser Ala Thr Val Asn Leu Thr
189         195                 200                 205
192 Val Ile Arg Cys Pro Gln Asp Thr Gly Gly Ile Asn Ile Pro Gly
193     210                 215                 220
196 Val Leu Ser Ser Leu Pro Ser Leu Gly Phe Ser Leu Pro Thr Trp Gly
197 225                 230                 235             240
200 Lys Val Gly Leu Gly Leu Ala Gly Thr Met Leu Leu Thr Pro Thr Cys
201             245                 250                 255
204 Thr Leu Thr Ile Arg Cys Cys Cys Arg Arg Arg Cys Cys Gly Cys
205             260                 265                 270
208 Asn Cys Cys Cys Arg Cys Cys Phe Cys Cys Arg Arg Lys Arg Gly Phe
209         275                 280                 285
212 Arg Ile Gln Phe Gln Lys Lys Ser Glu Lys Glu Lys Thr Asn Lys Glu
213     290                 295                 300
216 Thr Glu Thr Glu Ser Gly Asn Glu Asn Ser Gly Tyr Asn Ser Asp Glu
217 305                 310                 315             320
220 Gln Lys Thr Thr Asp Thr Ala Ser Leu Pro Pro Lys Ser Cys Glu Ser
221             325                 330                 335
224 Ser Asp Pro Glu Gln Arg Asn Ser Ser Cys Gly Pro Pro His Gln Arg
225             340                 345                 350
228 Ala Asp Gln Arg Pro Pro Arg Pro Ala Ser His Pro Gln Ala Ser Phe
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229         355              360              365
232 Asn Leu Ala Ser Pro Glu Lys Val Ser Asn Thr Thr Val Val
233     370              375              380
236 <210> SEQ ID NO: 3
237 <211> LENGTH: 1168
238 <212> TYPE: DNA
239 <213> ORGANISM: Homo sapiens
241 <220> FEATURE:
242 <221> NAME/KEY: CDS
243 <222> LOCATION: (8)..(1165)
245 <400> SEQUENCE: 3
246 agtgatc atg gtg gca gga gcc atg gaa aat aga gac cca ccc ggt tct    49
247         Met Val Ala Gly Ala Met Glu Asn Arg Asp Pro Pro Gly Ser
248         1               5                   10
250 ggg tct ggt aat gaa gtc ata gaa ggc ccc caa aat gca aga gtc ctg    97
251 Gly Ser Gly Asn Glu Val Ile Glu Gly Pro Gln Asn Ala Arg Val Leu
252 15              20                  25                  30
254 aag ggc tcc cag gct cgc ttc aac tgc acc gtc tcc cag ggc tgg aag   145
255 Lys Gly Ser Gln Ala Arg Phe Asn Cys Thr Val Ser Gln Gly Trp Lys
256             35                  40                  45
258 ctc atc atg tgg gct ctc agt gac atg gtg gtg cta agc gtc agg ccc   193
259 Leu Ile Met Trp Ala Leu Ser Asp Met Val Val Leu Ser Val Arg Pro
260             50                  55                  60
262 atg gag ccc atc atc acc aat gac cgc ttc acc tct cag agg tac gac   241
263 Met Glu Pro Ile Ile Thr Asn Asp Arg Phe Thr Ser Gln Arg Tyr Asp
264         65                  70                  75
266 cag ggc ggg aac ttc acc tcg gag atg atc atc cac aat gtg gag ccc   289
267 Gln Gly Gly Asn Phe Thr Ser Glu Met Ile Ile His Asn Val Glu Pro
268         80                  85                  90
270 agt gat tcg ggg aac atc aga tgc agc ctc cag aac agt cgc ctg cat   337
271 Ser Asp Ser Gly Asn Ile Arg Cys Ser Leu Gln Asn Ser Arg Leu His
272 95              100                 105                 110
274 gga tct gct tac ctt acc gtc caa gtt atg gga gag ctg ttc att ccc   385
275 Gly Ser Ala Tyr Leu Thr Val Gln Val Met Gly Glu Leu Phe Ile Pro
276             115                 120                 125
278 agt gtt aat ctt gta gtc gct gag aat gaa cct tgt gaa gtt act tgt   433
279 Ser Val Asn Leu Val Val Ala Glu Asn Glu Pro Cys Glu Val Thr Cys
280             130                 135                 140
282 cta ccc tca cac tgg acc tgg ctc ccg gat att tcc tgg gag ctc ggt   481
283 Leu Pro Ser His Trp Thr Trp Leu Pro Asp Ile Ser Trp Glu Leu Gly
284         145                 150                 155
286 ctc ctg gtc agc cat tca agc tat tat ttt gtt ccg gag ccc agc gac   529
287 Leu Leu Val Ser His Ser Ser Tyr Tyr Phe Val Pro Glu Pro Ser Asp
288         160                 165                 170
290 ctt caa agt gca gtg agc atc ctg gct ctg acc cca cag agc aat ggg   577
291 Leu Gln Ser Ala Val Ser Ile Leu Ala Leu Thr Pro Gln Ser Asn Gly
292 175             180                 185                 190
294 act ttg act tgc gtg gct acc tgg aag agc ctg aag gcc cgc aag tct   625
295 Thr Leu Thr Cys Val Ala Thr Trp Lys Ser Leu Lys Ala Arg Lys Ser
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296                195              200             205
298 gca act gta aat ctc act gtg att cgg tgt ccc caa gac act gga ggt    673
299 Ala Thr Val Asn Leu Thr Val Ile Arg Cys Pro Gln Asp Thr Gly Gly
300                210              215             220
302 ggt att aat att cca ggt gta tta tca agt tta ccg agt tta ggt ttt    721
303 Gly Ile Asn Ile Pro Gly Val Leu Ser Ser Leu Pro Ser Leu Gly Phe
304                225              230             235
306 tca ttg cct act tgg ggc aaa gtt gga ctt gga cta gca ggc acc atg    769
307 Ser Leu Pro Thr Trp Gly Lys Val Gly Leu Gly Leu Ala Gly Thr Met
308                240              245             250
310 ctt ctg acg ccg acg tgt act ctt aca ata cgc tgc tgc tgc tgc cgc    817
311 Leu Leu Thr Pro Thr Cys Thr Leu Thr Ile Arg Cys Cys Cys Cys Arg
312 255              260              265             270
314 cgt cgt tgt tgt ggc tgc aac tgc tgc tgc cgt tgt tgt ttc tgc tgt    865
315 Arg Arg Cys Cys Gly Cys Asn Cys Cys Cys Arg Cys Cys Phe Cys Cys
316                275              280             285
318 aga aga aaa aga gga ttt cgt att caa ttt caa aag aaa tct gaa aaa    913
319 Arg Arg Lys Arg Gly Phe Arg Ile Gln Phe Gln Lys Lys Ser Glu Lys
320                290              295             300
322 gag aag aca aac aaa gaa act gag aca gaa agt gga aat gaa aac tcc    961
323 Glu Lys Thr Asn Lys Glu Thr Glu Thr Glu Ser Gly Asn Glu Asn Ser
324                305              310             315
326 ggc tac aat tca gat gaa caa aag acc aca gac acc gct tct ctc cct    1009
327 Gly Tyr Asn Ser Asp Glu Gln Lys Thr Thr Asp Thr Ala Ser Leu Pro
328                320              325             330
330 ccc aaa tcc tgt gaa tcc agt gat cct gaa caa aga aac agt agc tgt    1057
331 Pro Lys Ser Cys Glu Ser Ser Asp Pro Glu Gln Arg Asn Ser Ser Cys
332 335              340              345             350
334 ggc cct cct cac cag cgg gct gat caa cgt cca ccc agg cca gca agt    1105
335 Gly Pro Pro His Gln Arg Ala Asp Gln Arg Pro Pro Arg Pro Ala Ser
336                355              360             365
338 cat cca cag gct tct ttt aat ctg gcc agt cct gag aag gtc agt aat    1153
339 His Pro Gln Ala Ser Phe Asn Leu Ala Ser Pro Glu Lys Val Ser Asn
340                370              375             380
342 aca act gta gta tag                                                1168
343 Thr Thr Val Val
344                385
347 <210> SEQ ID NO: 4
348 <211> LENGTH: 386
349 <212> TYPE: PRT
350 <213> ORGANISM: Homo sapiens
352 <400> SEQUENCE: 4
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355 1               5               10              15
358 Gly Asn Glu Val Ile Glu Gly Pro Gln Asn Ala Arg Val Leu Lys Gly
359                20              25              30
362 Ser Gln Ala Arg Phe Asn Cys Thr Val Ser Gln Gly Trp Lys Leu Ile
363                35              40              45
366 Met Trp Ala Leu Ser Asp Met Val Val Leu Ser Val Arg Pro Met Glu
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VERIFICATION SUMMARY   DATE: 12/19/2000
PATENT APPLICATION: US/09/729,264   TIME: 07:27:31

Input Set : A:\A-692.ST25.txt
Output Set: N:\CRF3\12192000\I729264.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number